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(1) GENERAL INFORMATION:

- (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5141 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vii) IMMEDIATE SOURCE:
  - (A) LIBRARY: TRISOMY 21 FETAL BRAIN cDNA LIBRARY
  - (B) CLONE: EHOC-1
- (viii) POSITION IN GENOME:
  - (A) CHROMOSOME/SEGMENT: 21q22.3
- (ix) FEATURE:
  - (A) NAME/KEY: CDS
  - (B) LOCATION: 157..3729

[illegible]

TTT	GTT	TTC	GAG	ATG	CTG	CAG	CAG	TTC	GAG	GAC	GCC	CTG	GTG	CAG	TAC	894
Phe	Val	Phe	Glu	Met	Leu	Gln	Gln	Phe	Glu	Asp	Ala	Leu	Val	Gln	Tyr	
			235						240					245		
GAC	GAA	CTG	GAC	GCC	CTC	TTC	TCT	CAG	TAT	GTG	GTC	AAC	TTC	GGG	GCC	942
Asp	Glu	Leu	Asp	Ala	Leu	Phe	Ser	Gln	Tyr	Val	Val	Asn	Phe	Gly	Ala	
			250					255					260			
GGG	GAT	GGT	GCC	AAC	TGG	CTG	ACT	TTT	TTC	TGC	CAG	CCA	GTG	AAG	AGC	990
Gly	Asp	Gly	Ala	Asn	Trp	Leu	Thr	Phe	Phe	Cys	Gln	Pro	Val	Lys	Ser	
		265					270					275				
TGG	AAC	GGA	TTG	ATC	CTC	CGA	AAA	CCC	ATA	GAT	ATG	GAG	AAG	CGG	GAA	1038
Trp	Asn	Gly	Leu	Ile	Leu	Arg	Lys	Pro	Ile	Asp	Met	Glu	Lys	Arg	Glu	
	280					285					290					
TCG	ATC	CAG	AGG	CGA	GAA	GCC	ACC	CTG	TTA	GAT	CTG	CGC	AGT	TAC	CTG	1086
Ser	Ile	Gln	Arg	Arg	Glu	Ala	Thr	Leu	Leu	Asp	Leu	Arg	Ser	Tyr	Leu	
	295				300					305					310	
TTC	TCT	CGC	CAG	TGC	ACC	TTG	CTG	CTC	TTC	CTG	CAG	AGG	CCG	TGG	GAG	1134
Phe	Ser	Arg	Gln	Cys	Thr	Leu	Leu	Leu	Phe	Leu	Gln	Arg	Pro	Trp	Glu	
			315						320					325		
GTG	GCC	CAG	CGC	GCC	CTA	GAG	CTG	CTG	CAC	AAC	TGC	GTG	CAG	GAA	CTG	1182
Val	Ala	Gln	Arg	Ala	Leu	Glu	Leu	Leu	His	Asn	Cys	Val	Gln	Glu	Leu	
			330				335						340			
AAG	CTC	TTA	GAA	GTC	TCT	GTC	CCA	CCT	GGT	GCT	CTG	GAC	TGC	TGG	GTG	1230
Lys	Leu	Leu	Glu	Val	Ser	Val	Pro	Pro	Gly	Ala	Leu	Asp	Cys	Trp	Val	
		345					350					355				
TTT	CTG	AGC	TGT	CTG	GAG	GTG	TTG	CAG	AGG	ATA	GAA	GGC	TGC	TGT	GAC	1278
Phe	Leu	Ser	Cys	Leu	Glu	Val	Leu	Gln	Arg	Ile	Glu	Gly	Cys	Cys	Asp	
	360					365					370					
CGG	GCA	CAG	ATC	GAC	TCA	AAC	ATT	GCC	CAC	ACT	GTG	GGG	CTA	TGG	AGC	1326
Arg	Ala	Gln	Ile	Asp	Ser	Asn	Ile	Ala	His	Thr	Val	Gly	Leu	Trp	Ser	
	375				380				385						390	
TAT	GCC	ACA	GAA	AAG	TTA	AAG	TCC	TTG	GGC	TAT	CTA	TGT	GGA	CTT	GTG	1374
Tyr	Ala	Thr	Glu	Lys	Leu	Lys	Ser	Leu	Gly	Tyr	Leu	Cys	Gly	Leu	Val	
			395					400						405		
TCA	GAG	AAA	GGA	CCT	AAC	TCA	GAA	GAT	CTC	AAC	AGG	ACA	GTT	GAC	CTT	1422
Ser	Glu	Lys	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Asn	Arg	Thr	Val	Asp	Leu	
			410					415					420			
TTG	GCA	GGT	TTG	GGA	GCT	GAG	CGA	CCA	GAA	ACA	GCC	AAC	ACA	GCT	CAG	1470
Leu	Ala	Gly	Leu	Gly	Ala	Glu	Arg	Pro	Glu	Thr	Ala	Asn	Thr	Ala	Gln	
		425					430					435				
AGT	CCT	TAT	AAG	AAA	CTG	AAA	GAA	GCA	TTA	TCG	TCA	GTG	GAA	GCT	TTT	1518
Ser	Pro	Tyr	Lys	Lys	Leu	Lys	Glu	Ala	Leu	Ser	Ser	Val	Glu	Ala	Phe	
	440					445					450					
GAA	AAA	CAC	TAC	TTA	GAT	TTG	TCC	CAT	GCC	ACC	ATT	GAA	ATG	TAT	ACA	1566
Glu	Lys	His	Tyr	Leu	Asp	Leu	Ser	His	Ala	Thr	Ile	Glu	Met	Tyr	Thr	
	455				460				465						470	
AGC	ATT	GGG	AGG	ATT	CGA	TCT	GCT	AAG	TTT	GTT	GGA	AAA	GAT	CTG	GCA	1614
Ser	Ile	Gly	Arg	Ile	Arg	Ser	Ala	Lys	Phe	Val	Gly	Lys	Asp	Leu	Ala	
			475					480						485		
GAG	TTT	TAC	ATG	AGG	AAA	AAG	GCT	CCA	CAA	AAG	GCA	GAA	ATC	TAT	CTT	1662
Glu	Phe	Tyr	Met	Arg	Lys	Lys	Ala	Pro	Gln	Lys	Ala	Glu	Ile	Tyr	Leu	
			490					495					500			

009907 "E26H460

CAA Gln	GGA Gly	GCA Ala	CTG Leu	AAA Lys	AAC Asn	TAC Tyr	CTG Leu	GCT Ala	GAG Glu	GGC Gly	TGG Trp	GCA Ala	CTC Leu	CCC Pro	ATC Ile	1710
505																
ACA Thr	CAC His	ACA Thr	AGG Arg	AAG Lys	CAG Gln	CTG Leu	GCC Ala	GAA Glu	TGT Cys	CAA Gln	AAG Lys	CAC His	CTT Leu	GGA Gly	CAA Gln	1758
520																
ATT Ile	GAA Glu	AAC Asn	TAC Tyr	CTG Leu	CAG Gln	ACC Thr	AGC Ser	AGC Ser	CTC Leu	TTA Leu	GCC Ala	AGT Ser	GAC Asp	CAC His	CAC His	1806
535																
CTC Leu	ACT Thr	GAA Glu	GAG Glu	GAG Glu	CGC Arg	AAG Lys	CAC His	TTC Phe	TGC Cys	CAG Gln	GAG Glu	ATA Ile	CTT Leu	GAC Asp	TTT Phe	1854
555																
GCC Ala	AGC Ser	CAG Gln	CCG Pro	TCA Ser	GAC Asp	AGC Ser	CCA Pro	GGT Gly	CAT His	AAG Lys	ATA Ile	GTG Val	CTA Leu	CCC Pro	ATG Met	1902
570																
CAT His	TCC Ser	TTT Phe	GCA Ala	CAA Gln	CTG Leu	CGA Arg	GAT Asp	CTC Leu	CAT His	TTT Phe	GAT Asp	CCC Pro	TCC Ser	AAT Asn	GCC Ala	1950
585																
GTG Val	GTC Val	CAC His	GTG Val	GGC Gly	GGC Gly	GTT Val	TTG Leu	TGC Cys	GTT Val	GAG Glu	ATA Ile	ACC Thr	ATG Met	TAC Tyr	AGC Ser	1998
600																
CAG Gln	ATG Met	CCT Pro	GTG Val	CCT Pro	GTT Val	CAC His	GTG Val	GAG Glu	CAG Gln	ATT Ile	GTG Val	GTC Val	AAT Asn	GTC Val	CAC His	2046
615																
TTC Phe	AGC Ser	ATT Ile	GAG Glu	AAA Lys	AAC Asn	AGC Ser	TAC Tyr	CGG Arg	AAG Lys	ACT Thr	GCG Ala	GAG Glu	TGG Trp	CTT Leu	ACC Thr	2094
635																
AAG Lys	CAC His	AAG Lys	ACG Thr	TCC Ser	AAT Asn	GGG Gly	ATC Ile	ATT Ile	AAC Asn	TTT Phe	CCA Pro	CCC Pro	GAG Glu	ACC Thr	GCA Ala	2142
650																
CCT Pro	TTC Phe	CCT Pro	GTA Val	TCC Ser	CAA Gln	AAC Asn	AGT Ser	TTG Leu	CCC Pro	GCG Ala	CTG Leu	GAG Glu	TTG Leu	TAT Tyr	GAA Glu	2190
665																
ATG Met	TTT Phe	GAG Glu	AGA Arg	AGC Ser	CCA Pro	TCT Ser	GAT Asp	AAC Asn	TCC Ser	TTG Leu	AAC Asn	ACG Thr	ACT Thr	GGG Gly	ATT Ile	2238
680																
ATC Ile	TGC Cys	AGA Arg	AAC Asn	GTC Val	CAC His	ATG Met	CTC Leu	CTG Leu	AGA Arg	AGG Arg	CAG Gln	GAG Glu	AGC Ser	AGC Ser	TCC Ser	2286
695																
TCT Ser	CTA Leu	GAG Glu	ATG Met	CCC Pro	TCA Ser	GGG Gly	GTG Val	GCT Ala	CTG Leu	GAG Glu	GAG Glu	GGT Gly	GCC Ala	CAC His	GTG Val	2334
715																
CTG Leu	AGG Arg	TGC Cys	AGC Ser	CAC His	GTG Val	ACC Thr	CTG Leu	GAA Glu	CCA Pro	GGG Gly	GCC Ala	AAC Asn	CAG Gln	ATA Ile	ACA Thr	2382
730																
TTC Phe	AGG Arg	ACT Thr	CAG Gln	GCC Ala	AAG Lys	GAA Glu	CCT Pro	GGA Gly	ACG Thr	TAT Tyr	ACA Thr	CTC Leu	AGG Arg	CAG Gln	CTG Leu	2430
745																
TGC Cys	GCC Ala	TCG Ser	GTG Val	GGC Gly	TCC Ser	GTG Val	TGG Trp	TTC Phe	GTC Val	CTC Leu	CCT Pro	CAC His	ATC Ile	TAC Tyr	CCC Pro	2478
760																
765																
770																

ATT GTG CAG TAC GAC GTG TAC TCA CAG GAG CCC CAG CTG CAC GTG GAG Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu Pro Gln Leu His Val Glu 775 780 785 790	2526
CCG CTG GCT GAT AGC CTT CTG GCA GGC ATT CCT CAG AGA GTC AAG TTC Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile Pro Gln Arg Val Lys Phe 795 800 805	2574
ACT GTC ACT ACC GGC CAT GAT ACG ATA AAG AAT GGA GAC AGC CTG CAG Thr Val Thr Thr Gly His Asp Thr Ile Lys Asn Gly Asp Ser Leu Gln 810 815 820	2622
CTT AGC AAT GCC GAA GCC ATG CTC ATC CTG TGC CAG GCG GAG AGC AGG Leu Ser Asn Ala Glu Ala Met Leu Ile Leu Cys Gln Ala Glu Ser Arg 825 830 835	2670
GCT GTG GTC TAC TCC AAC ACG AGA GAA CAG TCT TCT GAG GCC GCG CTC Ala Val Val Tyr Ser Asn Thr Arg Glu Gln Ser Ser Glu Ala Ala Leu 840 845 850	2718
CGG ATT CAG TCC TCC GAC AAG GTC ACG AGC ATC AGT CTG CCT GTT GCG Arg Ile Gln Ser Ser Asp Lys Val Thr Ser Ile Ser Leu Pro Val Ala 855 860 865 870	2766
CCT GCG TAC CAC GTG ATC GAA TTT GAA CTG GAA GTT CTC TCT TTA CCT Pro Ala Tyr His Val Ile Glu Phe Glu Leu Glu Val Leu Ser Leu Pro 875 880 885	2814
TCA GCC CCA GCA CTC GGA GGG GAG AGT GAC ATG CTG GGG ATG GCA GAG Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp Met Leu Gly Met Ala Glu 890 895 900	2862
CCC CAC AGG AAG CAT AAG GAC AAA CAG AGA ACT GGC CGC TGC ATG GTT Pro His Arg Lys His Lys Asp Lys Gln Arg Thr Gly Arg Cys Met Val 905 910 915	2910
ACC ACA GAC CAC AAA GTG TCG ATT GAC TGC CCG TGG TCC ATC TAC TCC Thr Thr Asp His Lys Val Ser Ile Asp Cys Pro Trp Ser Ile Tyr Ser 920 925 930	2958
ACA GTC ATC GCA CTG ACC TTC AGC GTA CCC TTC AGG ACC ACA CAC AGC Thr Val Ile Ala Leu Thr Phe Ser Val Pro Phe Arg Thr Thr His Ser 935 940 945 950	3006
CTC CTG TCC TCA GGA ACA CGG AAA TAT GTT CAA GTT TGT GTC CAG AAT Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val Gln Val Cys Val Gln Asn 955 960 965	3054
TTG TCA GAA CTT GAC TTT CAG CTG TCA GAT AGT TAT CTT GTA GAT ACC Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp Ser Tyr Leu Val Asp Thr 970 975 980	3102
GGT GAT AGT ACC GAC CTG CAA CTA GTA CCA CTG AAC ACG CAG TCC CAG Gly Asp Ser Thr Asp Leu Gln Leu Val Pro Leu Asn Thr Gln Ser Gln 985 990 995	3150
CAG CCC ATC TAC AGC AAG CAG TCG GTG TTC TTC GTC TGG GAA CTC AAG Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe Phe Val Trp Glu Leu Lys 1000 1005 1010	3198
TGG ACA GAA GAG CCT CCC CCT TCT CTG CAT TGC CGG TTC TCT GTT GGA Trp Thr Glu Glu Pro Pro Ser Leu His Cys Arg Phe Ser Val Gly 1015 1020 1025 1030	3246
TTT TCC CCA GCT TCT GAG GAA CAG CTG TCT ATC TCC TTA AAG CCG TAT Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser Ile Ser Leu Lys Pro Tyr 1035 1040 1045	3294

ACT TAT GAA TTT AAA GTG GAA AAT TTT TTT ACA TTA TAC AAC GTG AAG 3342  
 Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe Thr Leu Tyr Asn Val Lys  
 1050 1055 1060

GCT GAG ATC TTT CCC CCT TCG GGA ATG GAG TAT TGC AGA ACA GGC TCC 3390  
 Ala Glu Ile Phe Pro Pro Ser Gly Met Glu Tyr Cys Arg Thr Gly Ser  
 1065 1070 1075

CTC TGC TCC CTG GAG GTT TTG ATC ACG AGG CTC TCA GAC CTC TTG GAG 3438  
 Leu Cys Ser Leu Glu Val Leu Ile Thr Arg Leu Ser Asp Leu Leu Glu  
 1080 1085 1090

GTG GAT AAA GAT GAA GCA CTG ACT GAA TCT GAT GAG CAT TTT TCG ACA 3486  
 Val Asp Lys Asp Glu Ala Leu Thr Glu Ser Asp Glu His Phe Ser Thr  
 1095 1100 1105 1110

AAG CTT ATG TAT GAA GTT GTC GAC AAC AGT AGC AAC TGG GCA GTG TGT 3534  
 Lys Leu Met Tyr Glu Val Val Asp Asn Ser Ser Asn Trp Ala Val Cys  
 1115 1120 1125

GGG AAA AGC TGC GGT GTC ATC TCC ATG CCA GTG GCT GCT CGG GCC ACT 3582  
 Gly Lys Ser Cys Gly Val Ile Ser Met Pro Val Ala Ala Arg Ala Thr  
 1130 1135 1140

CAC AGG GTC CAC ATG GAA GTG ATG CCG CTC TTC GCC GGG TAT CTC CCC 3630  
 His Arg Val His Met Glu Val Met Pro Leu Phe Ala Gly Tyr Leu Pro  
 1145 1150 1155

CTG CCC GAC GTC AGG CTG TTC AAG TAC CTC CCC CAT CAT TCT GCA CAC 3678  
 Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu Pro His His Ser Ala His  
 1160 1165 1170

TCC TCC CAA CTG GAC GCT GAC AGC TGG ATA GAA AAC GCA GCC TGT CAG 3726  
 Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile Glu Asn Ala Ala Cys Gln  
 1175 1180 1185 1190

TAGACAAGCA CGGGGACGAC CAGCCGGACA GCAGCAGCCT CAAGAGCAGG GGCAGCGTGC 3786

ATTCGGCCTG CAGCAGCGAG CACAAAGGCC TACCCATGCC CCGGCTGCAG GCACTGCCGG 3846

CCGGCCAGGT CTTCAACTCC AGCTCGGGCA CACAAGTCCT GGTCATCCCC AGCCAAGATG 3906

ACCACGTCCT GGAAGTCAGT GTAACATGAC AACGCCAGGG TGAACACACG CCACTTCCCCA 3966

GCTAGGAGTG CACTTTATGG GACTGTGACT GGACTCTTCC GTTCTGGCTC CAGCCAGACC 4026

TTCAGTGGTC CTGCCTGGCC GTGGGGACAT CAGAGAGTGT CATCACGCAG CTGGCCAGCT 4086

GAGTTCTGTT GTTGTTTTCA TGCCGCCTGT GATCTCAGAT TCCTGCTTTT CTCACCCCGT 4146

CCCCATGCTG GTGTCCGACG CCGCTTACTC AGAGCCCTGG CCTCCCTCCC CCTACCTCAC 4206

ACGCTGCTCA TGAAAGTTTC CACCCACGCT GTCTCCACGG AACAGCCTCC GTCTGCTGGC 4266

TCTTCGTGGA AGGCCATTTG TCTTTCAGGT AGACACTCAG CAGCCCTCAC GGTCTTAGTG 4326

ACGTGTGTGC CTTTCTGGTC ACACAGCTGC CCAGTTTCCT GATCGGGGTG GATTTGTGTC 4386

CCCTAAGGGG TAAACAGCC GTTTACCGCA GATCCTCTCA TACACCTTC TAGGGGAGGC 4446

GGGTGGGGGA GGGAGGGATC ATAACCCCTT CTGTGCCTTG GGATGCCGGA GCTGGGGGAC 4506

CTGGAGGCCC ATCAGCCGGA GCCACGTGAA AGGTACTGAA GAAAGCTGAG ACCCGGCTGT 4566

GAGGAGCGCC TCAGCGGTGA GGTGGTTTAG GGATAAATGT TTCTGGAACC CTGTGGTCCC 4626

CCATAATGTT GATAGATATC ATATGCACTG GGAGTTAAAT ATATTTAATT TAATGATCAT 4686

003227 E 220400

TATATATGTG GGGGTTAATA TGTTGTTTTT CTGTCCCTTT AAAGTCTTTA CATGTAATTG 4746  
 TAGCTGTATA ATCGTTATTT TTCTTTTGCA TCTTAAGTCT TAGAAATTAA GATATTCCAT 4806  
 CGTGAGGATG AGAGAGGTCC TCAGTGTGTT TTTGGTCTGG TTGTAGGGAA GGA CTCAAGT 4866  
 CCTGGAATGT CCTCCACTGG TCTACTGAGT TGCAGTCACA CTGTTCCAAT GGATTATTTG 4926  
 CTTTCGGTTG TAAATTTAAT TGTACATATG GTTGATTTAT TATTTTAAAA AATACAGACT 4986  
 AACTGATGTA ATGTTTATGT ATAAGTTGCA CCAAAAATCA AGGACAAAAA TAAGTGTGTT 5046  
 TGTTTTTACA GGTGTGAAAG TCACAGCTTG TAAATAAGTG TTGTATGTAT TAAACCTTTT 5106  
 CCAGTTCTCC AAAAAAAAAA AAAAAAAAAA AAAAA 5141

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1190 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Ala Ser Glu Glu Pro Leu Pro Pro Val Ile Tyr Thr Met Glu  
 1 5 10 15  
 Asn Lys Pro Ile Val Thr Cys Ala Gly Asp Gln Asn Leu Phe Thr Ser  
 20 25 30  
 Val Tyr Pro Thr Leu Ser Gln Gln Leu Pro Arg Glu Pro Met Glu Trp  
 35 40 45  
 Arg Arg Ser Tyr Gly Arg Ala Pro Lys Met Ile His Leu Glu Ser Asn  
 50 55 60  
 Phe Val Gln Phe Lys Glu Glu Leu Leu Pro Lys Glu Gly Asn Lys Ala  
 65 70 75 80  
 Leu Leu Thr Phe Pro Phe Leu His Ile Tyr Trp Thr Glu Cys Cys Asp  
 85 90 95  
 Thr Glu Val Tyr Lys Ala Thr Val Lys Asp Asp Leu Thr Lys Trp Gln  
 100 105 110  
 Asn Val Leu Lys Ala His Ser Ser Val Asp Trp Leu Ile Val Ile Val  
 115 120 125  
 Glu Asn Asp Ala Lys Lys Lys Asn Lys Thr Asn Ile Leu Pro Arg Thr  
 130 135 140  
 Ser Ile Val Asp Lys Ile Arg Asn Asp Phe Cys Asn Lys Gln Ser Asp  
 145 150 155 160  
 Arg Cys Val Val Leu Ser Asp Pro Leu Lys Asp Ser Ser Arg Thr Gln  
 165 170 175  
 Glu Ser Trp Asn Ala Phe Leu Thr Lys Leu Arg Thr Leu Leu Leu Met  
 180 185 190  
 Ser Phe Thr Lys Asn Leu Gly Lys Phe Glu Asp Asp Met Arg Thr Leu  
 195 200 205



Arg	Glu	Lys	Arg	Thr	Glu	Pro	Gly	Trp	Ser	Phe	Cys	Glu	Tyr	Phe	Met
210						215					220				
Val	Gln	Glu	Glu	Leu	Ala	Phe	Val	Phe	Glu	Met	Leu	Gln	Gln	Phe	Glu
225					230					235					240
Asp	Ala	Leu	Val	Gln	Tyr	Asp	Glu	Leu	Asp	Ala	Leu	Phe	Ser	Gln	Tyr
				245					250					255	
Val	Val	Asn	Phe	Gly	Ala	Gly	Asp	Gly	Ala	Asn	Trp	Leu	Thr	Phe	Phe
			260					265					270		
Cys	Gln	Pro	Val	Lys	Ser	Trp	Asn	Gly	Leu	Ile	Leu	Arg	Lys	Pro	Ile
		275					280					285			
Asp	Met	Glu	Lys	Arg	Glu	Ser	Ile	Gln	Arg	Arg	Glu	Ala	Thr	Leu	Leu
	290					295					300				
Asp	Leu	Arg	Ser	Tyr	Leu	Phe	Ser	Arg	Gln	Cys	Thr	Leu	Leu	Leu	Phe
305					310					315					320
Leu	Gln	Arg	Pro	Trp	Glu	Val	Ala	Gln	Arg	Ala	Leu	Glu	Leu	Leu	His
				325					330					335	
Asn	Cys	Val	Gln	Glu	Leu	Lys	Leu	Leu	Glu	Val	Ser	Val	Pro	Pro	Gly
			340					345					350		
Ala	Leu	Asp	Cys	Trp	Val	Phe	Leu	Ser	Cys	Leu	Glu	Val	Leu	Gln	Arg
		355					360					365			
Ile	Glu	Gly	Cys	Cys	Asp	Arg	Ala	Gln	Ile	Asp	Ser	Asn	Ile	Ala	His
	370					375					380				
Thr	Val	Gly	Leu	Trp	Ser	Tyr	Ala	Thr	Glu	Lys	Leu	Lys	Ser	Leu	Gly
385					390					395					400
Tyr	Leu	Cys	Gly	Leu	Val	Ser	Glu	Lys	Gly	Pro	Asn	Ser	Glu	Asp	Leu
				405					410					415	
Asn	Arg	Thr	Val	Asp	Leu	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Arg	Pro	Glu
			420					425					430		
Thr	Ala	Asn	Thr	Ala	Gln	Ser	Pro	Tyr	Lys	Lys	Leu	Lys	Glu	Ala	Leu
		435					440					445			
Ser	Ser	Val	Glu	Ala	Phe	Glu	Lys	His	Tyr	Leu	Asp	Leu	Ser	His	Ala
	450					455					460				
Thr	Ile	Glu	Met	Tyr	Thr	Ser	Ile	Gly	Arg	Ile	Arg	Ser	Ala	Lys	Phe
465					470					475					480
Val	Gly	Lys	Asp	Leu	Ala	Glu	Phe	Tyr	Met	Arg	Lys	Lys	Ala	Pro	Gln
				485					490					495	
Lys	Ala	Glu	Ile	Tyr	Leu	Gln	Gly	Ala	Leu	Lys	Asn	Tyr	Leu	Ala	Glu
			500					505					510		
Gly	Trp	Ala	Leu	Pro	Ile	Thr	His	Thr	Arg	Lys	Gln	Leu	Ala	Glu	Cys
							520					525			
Gln	Lys	His	Leu	Gly	Gln	Ile	Glu	Asn	Tyr	Leu	Gln	Thr	Ser	Ser	Leu
	530					535					540				
Leu	Ala	Ser													

Gln Glu Ile Leu Asp Phe Ala Ser Gln Pro Ser Asp Ser Pro Gly His  
 565 570 575  
 Lys Ile Val Leu Pro Met His Ser Phe Ala Gln Leu Arg Asp Leu His  
 580 585 590  
 Phe Asp Pro Ser Asn Ala Val Val His Val Gly Gly Val Leu Cys Val  
 595 600 605  
 Glu Ile Thr Met Tyr Ser Gln Met Pro Val Pro Val His Val Glu Gln  
 610 615 620  
 Ile Val Val Asn Val His Phe Ser Ile Glu Lys Asn Ser Tyr Arg Lys  
 625 630 635 640  
 Thr Ala Glu Trp Leu Thr Lys His Lys Thr Ser Asn Gly Ile Ile Asn  
 645 650 655  
 Phe Pro Pro Glu Thr Ala Pro Phe Pro Val Ser Gln Asn Ser Leu Pro  
 660 665 670  
 Ala Leu Glu Leu Tyr Glu Met Phe Glu Arg Ser Pro Ser Asp Asn Ser  
 675 680 685  
 Leu Asn Thr Thr Gly Ile Ile Cys Arg Asn Val His Met Leu Leu Arg  
 690 695 700  
 Arg Gln Glu Ser Ser Ser Ser Leu Glu Met Pro Ser Gly Val Ala Leu  
 705 710 715 720  
 Glu Glu Gly Ala His Val Leu Arg Cys Ser His Val Thr Leu Glu Pro  
 725 730 735  
 Gly Ala Asn Gln Ile Thr Phe Arg Thr Gln Ala Lys Glu Pro Gly Thr  
 740 745 750  
 Tyr Thr Leu Arg Gln Leu Cys Ala Ser Val Gly Ser Val Trp Phe Val  
 755 760 765  
 Leu Pro His Ile Tyr Pro Ile Val Gln Tyr Asp Val Tyr Ser Gln Glu  
 770 775 780  
 Pro Gln Leu His Val Glu Pro Leu Ala Asp Ser Leu Leu Ala Gly Ile  
 785 790 795 800  
 Pro Gln Arg Val Lys Phe Thr Val Thr Thr Gly His Asp Thr Ile Lys  
 805 810 815  
 Asn Gly Asp Ser Leu Gln Leu Ser Asn Ala Glu Ala Met Leu Ile Leu  
 820 825 830  
 Cys Gln Ala Glu Ser Arg Ala Val Val Tyr Ser Asn Thr Arg Glu Gln  
 835 840 845  
 Ser Ser Glu Ala Ala Leu Arg Ile Gln Ser Ser Asp Lys Val Thr Ser  
 850 855 860  
 Ile Ser Leu Pro Val Ala Pro Ala Tyr His Val Ile Glu Phe Glu Leu  
 865 870 875 880  
 Glu Val Leu Ser Leu Pro Ser Ala Pro Ala Leu Gly Gly Glu Ser Asp  
 885 890 895  
 Met Leu Gly Met Ala Glu Pro His Arg Lys His Lys Asp Lys Gln Arg  
 900 905 910

009227 "E.E.64460

Thr Gly Arg Cys Met Val Thr Thr Asp His Lys Val Ser Ile Asp Cys  
 915 920 925  
 Pro Trp Ser Ile Tyr Ser Thr Val Ile Ala Leu Thr Phe Ser Val Pro  
 930 935 940  
 Phe Arg Thr Thr His Ser Leu Leu Ser Ser Gly Thr Arg Lys Tyr Val  
 945 950 955 960  
 Gln Val Cys Val Gln Asn Leu Ser Glu Leu Asp Phe Gln Leu Ser Asp  
 965 970 975  
 Ser Tyr Leu Val Asp Thr Gly Asp Ser Thr Asp Leu Gln Leu Val Pro  
 980 985 990  
 Leu Asn Thr Gln Ser Gln Gln Pro Ile Tyr Ser Lys Gln Ser Val Phe  
 995 1000 1005  
 Phe Val Trp Glu Leu Lys Trp Thr Glu Glu Pro Pro Pro Ser Leu His  
 1010 1015 1020  
 Cys Arg Phe Ser Val Gly Phe Ser Pro Ala Ser Glu Glu Gln Leu Ser  
 1025 1030 1035 1040  
 Ile Ser Leu Lys Pro Tyr Thr Tyr Glu Phe Lys Val Glu Asn Phe Phe  
 1045 1050 1055  
 Thr Leu Tyr Asn Val Lys Ala Glu Ile Phe Pro Pro Ser Gly Met Glu  
 1060 1065 1070  
 Tyr Cys Arg Thr Gly Ser Leu Cys Ser Leu Glu Val Leu Ile Thr Arg  
 1075 1080 1085  
 Leu Ser Asp Leu Leu Glu Val Asp Lys Asp Glu Ala Leu Thr Glu Ser  
 1090 1095 1100  
 Asp Glu His Phe Ser Thr Lys Leu Met Tyr Glu Val Val Asp Asn Ser  
 1105 1110 1115 1120  
 Ser Asn Trp Ala Val Cys Gly Lys Ser Cys Gly Val Ile Ser Met Pro  
 1125 1130 1135  
 Val Ala Ala Arg Ala Thr His Arg Val His Met Glu Val Met Pro Leu  
 1140 1145 1150  
 Phe Ala Gly Tyr Leu Pro Leu Pro Asp Val Arg Leu Phe Lys Tyr Leu  
 1155 1160 1165  
 Pro His His Ser Ala His Ser Ser Gln Leu Asp Ala Asp Ser Trp Ile  
 1170 1175 1180  
 Glu Asn Ala Ala Cys Gln  
 1185 1190

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Moraxella bovis*

(C) INDIVIDUAL ISOLATE: MboI linker

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CCTGATGCTC GAGTGAATTC

20

1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Discussion**  
 6. **Conclusion**  
 7. **References**  
 8. **Appendix**  
 9. **Notes**  
 10. **Tables**  
 11. **Figures**  
 12. **Supplementary Materials**  
 13. **Author Contributions**  
 14. **Funding**  
 15. **Conflict of Interest**  
 16. **Publisher's Note**  
 17. **Copyright**  
 18. **Disclaimer**  
 19. **References**  
 20. **Appendix**  
 21. **Notes**  
 22. **Tables**  
 23. **Figures**  
 24. **Supplementary Materials**  
 25. **Author Contributions**  
 26. **Funding**  
 27. **Conflict of Interest**  
 28. **Publisher's Note**  
 29. **Copyright**  
 30. **Disclaimer**